

Convex Usage Request

This form should be completed by Helix users who wish to register to use the NIH Convex system for the first time or by current Convex users who are required to provide justification for their continued use of the Convex.

Compute-intensive work requiring large memory or vector processing should reside on the Convex system. Examples include computational chemistry programs (Gaussian, MOPAC, CHARMm), mathematical and statistical programs that require large amounts of memory (MATLAB, Mathematica), and user-developed programs which currently run on the Convex system.

User Information:

- Name:
- Institute:
- NIH Address:
- Telephone:
- Helix User Name:

Just

(Include a brief description of your requirements for using the Convex system):

Categories

(In order to help us categorize the Convex workload, please check whichever apply to your own usage):

- | | |
|---|--|
| <input type="checkbox"/> Crystallography or NMR Spectroscopy | <input type="checkbox"/> Cell modelling |
| <input type="checkbox"/> Molecular Dynamics | <input type="checkbox"/> Mathematical Modelling |
| <input type="checkbox"/> Molecular Modelling | <input type="checkbox"/> Image processing |
| <input type="checkbox"/> Quantum calculations | <input type="checkbox"/> Graphics or Visualization |
| <input type="checkbox"/> RNA secondary structure | <input type="checkbox"/> Statistics |
| <input type="checkbox"/> Sequence Analysis, Protein or Nucleic Acid | <input type="checkbox"/> Physical Chemistry |
| <input type="checkbox"/> Genetics | <input type="checkbox"/> Other: |
| <input type="checkbox"/> Neuro-modelling | |